

APPROVED BY DRAFTSMAN	O.G. FIG.
	CLASS SUBCLASS

0916754

Systematic Gene Search in the Incyte LifeSeq Database

00000000000000000000000000000000

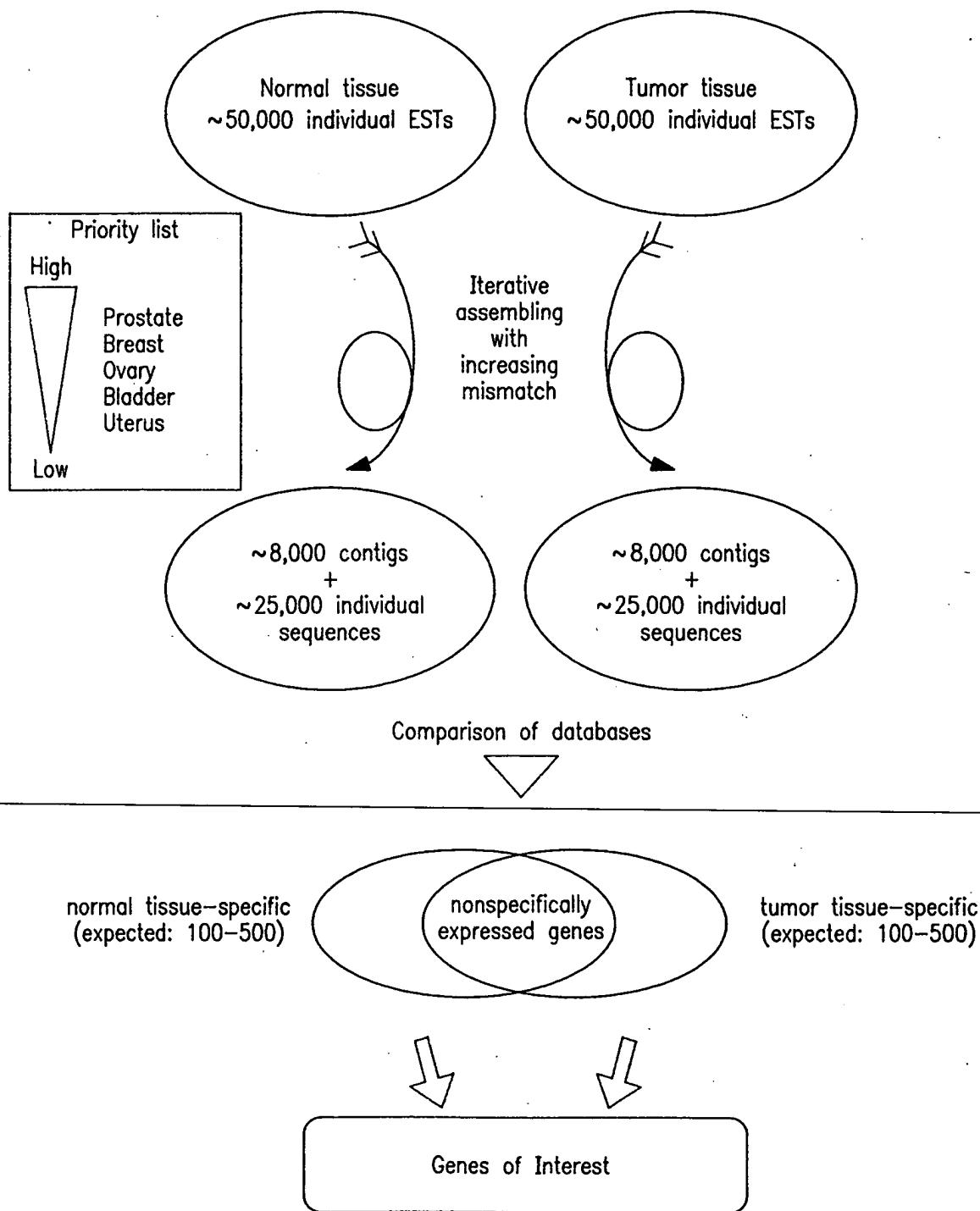


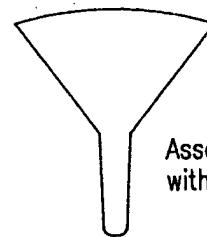
FIG. 1

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09/673400

Principle of EST Assembly

~50,000 ESTs per tissue



Assembly at 0% mismatch
with GAP4 (Staden)

Contigs

Individual Sequences

Contigs increasing in
number and length

Iterative assembly with
increasing mismatch
(1%, 2%, 4%)

5000-6000 Contigs

~25,000 other individual
sequences

~30,000 consensus-
sequences per tissue

FIG. 2a

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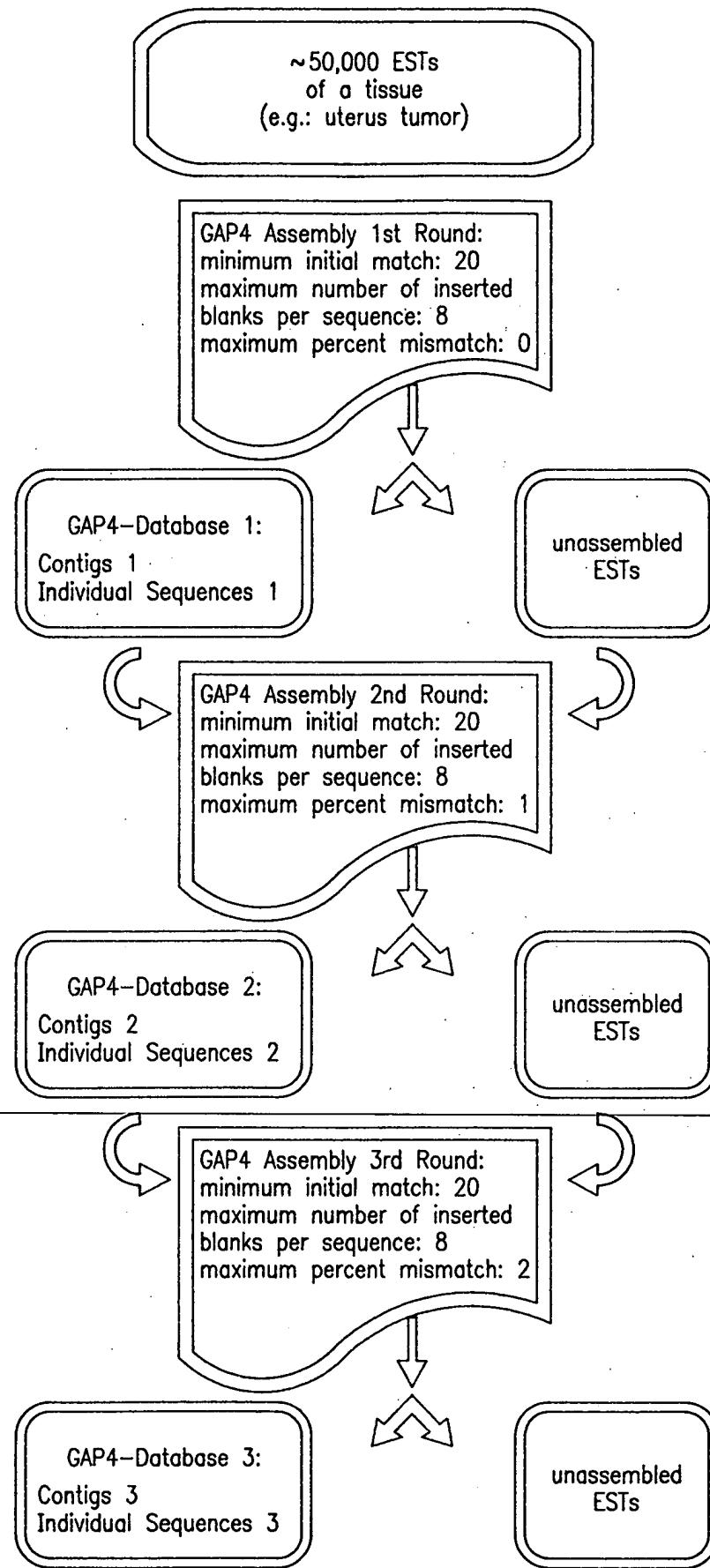


FIG. 2b-I

00000000000000000000000000000000

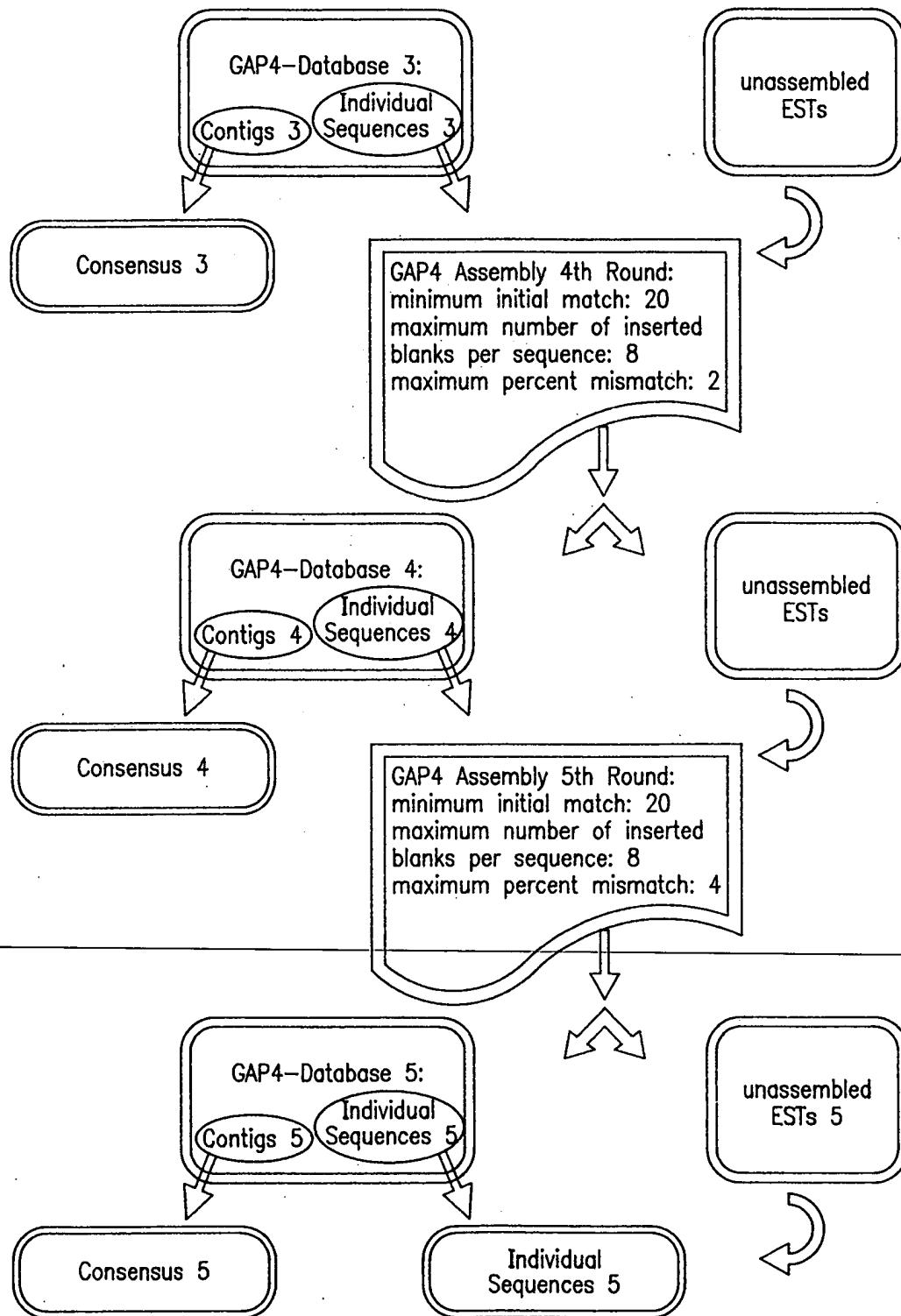


FIG. 2b-2

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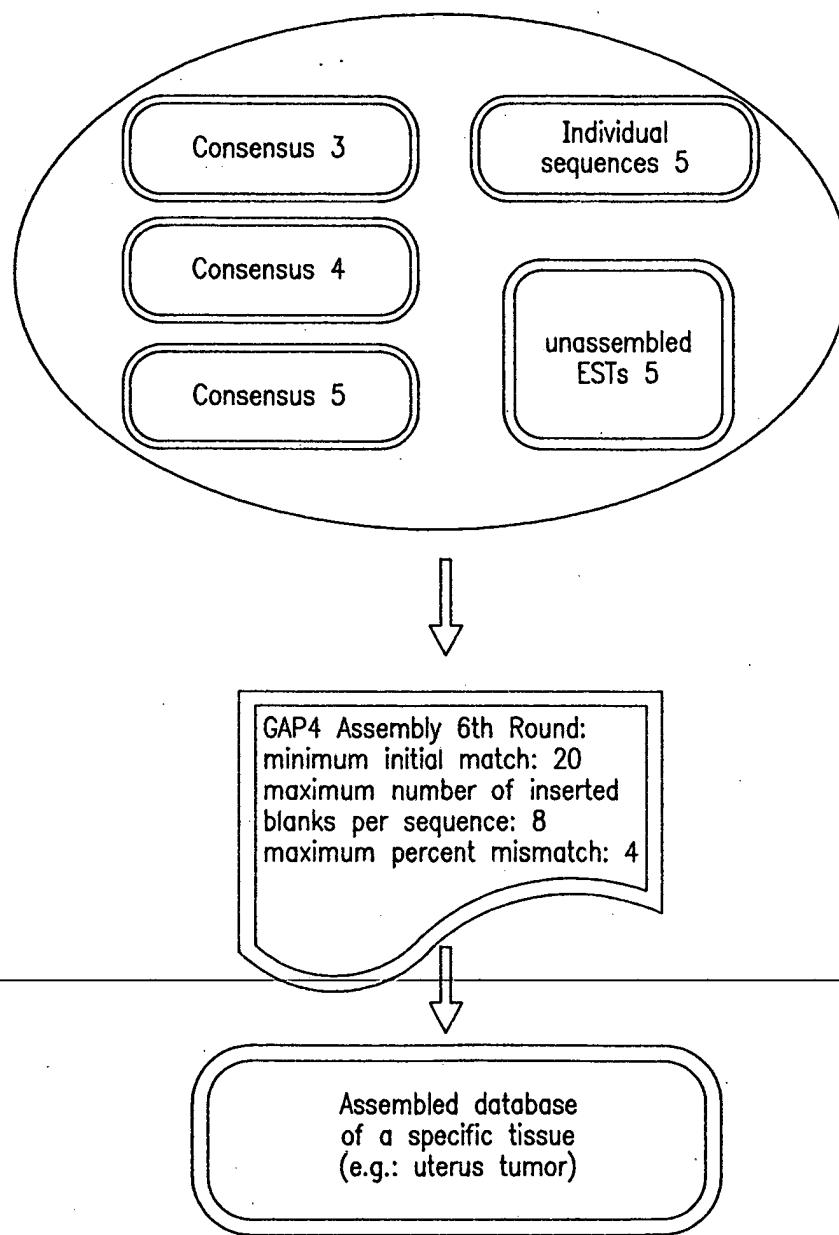


FIG. 2b-3

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DRAFTSMAN: "KELLY" 091673461

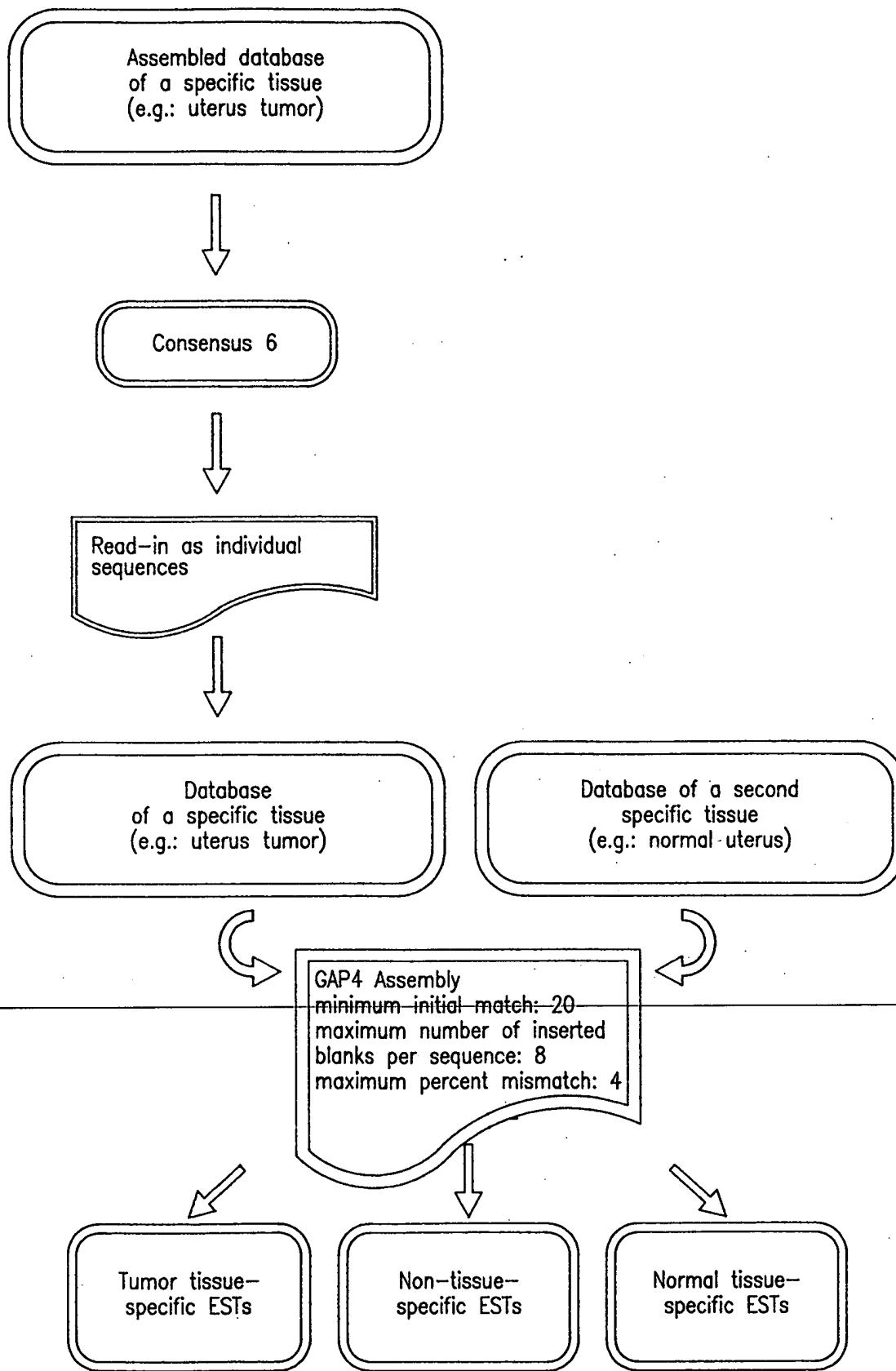


FIG. 2b-4

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In silico subtraction of gene expression in various tissues

~30,000 consensus sequences
normal tissue

~30,000 consensus sequences
tumor tissue

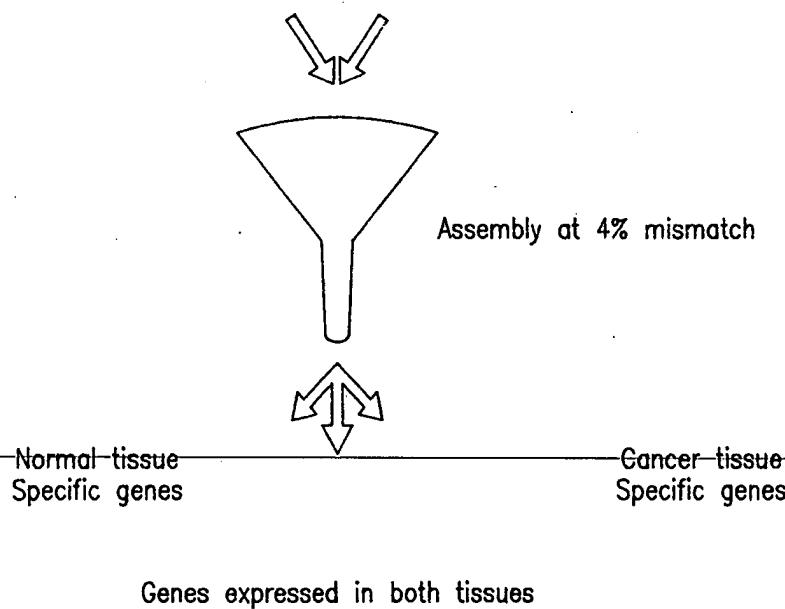
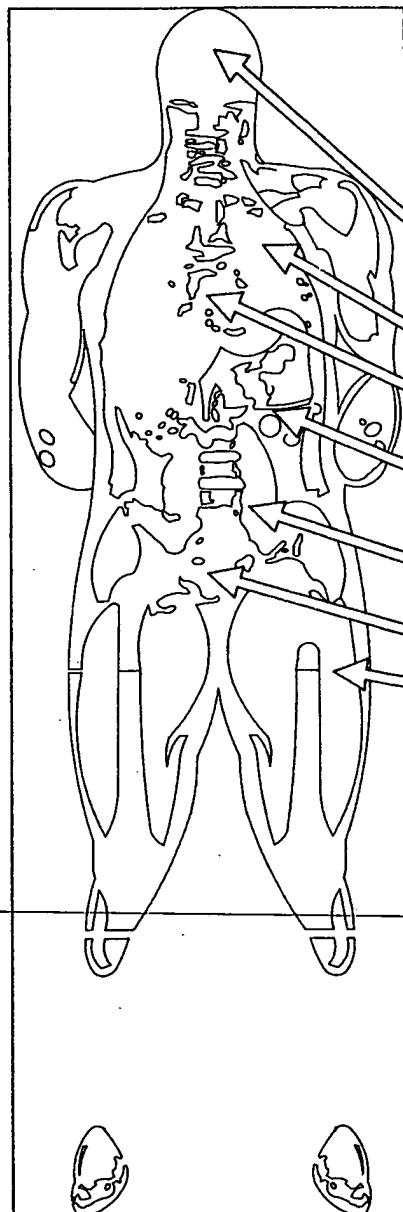


FIG. 3

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Genes of interest

Determination of tissue-specific
expression via electronic
Northern (INCYTE LifeSeq
and public EST databases)

Candidate genes for tumor
suppressors or tumor activators

FIG. 4a

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00224456224456

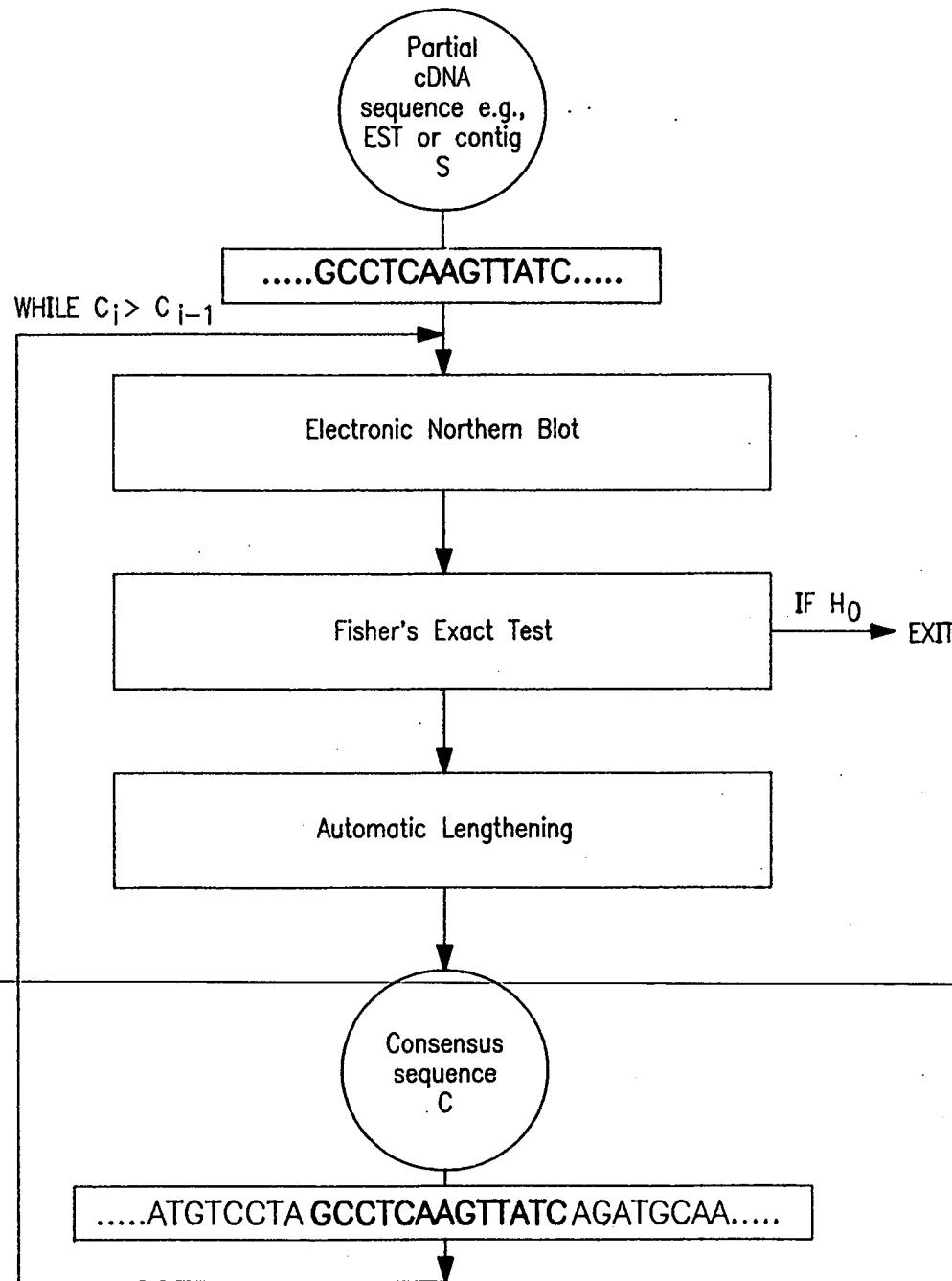


FIG. 4b

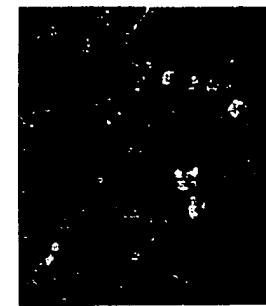
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Isolation of genomic BAC and PAC clones

Chromosomal clone localization via FISH



Hybridization signal



Sequencing of clones that are located in regions that have chromosomal deletions in prostate and breast cancer leads to identification of candidate genes



Confirmation of candidate genes by screening of mutations and/or deletions in cancer tissues

FIG. 5